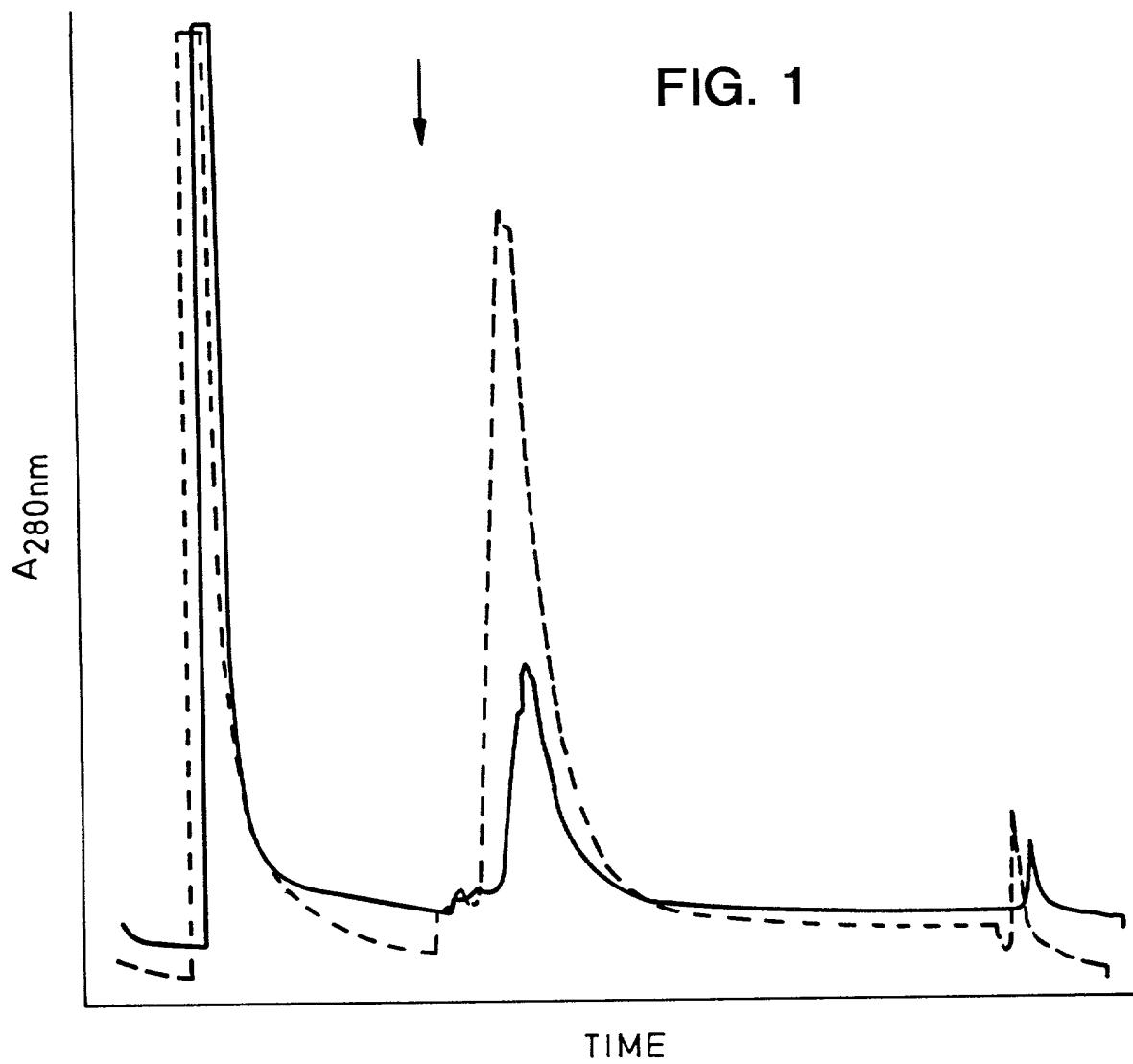
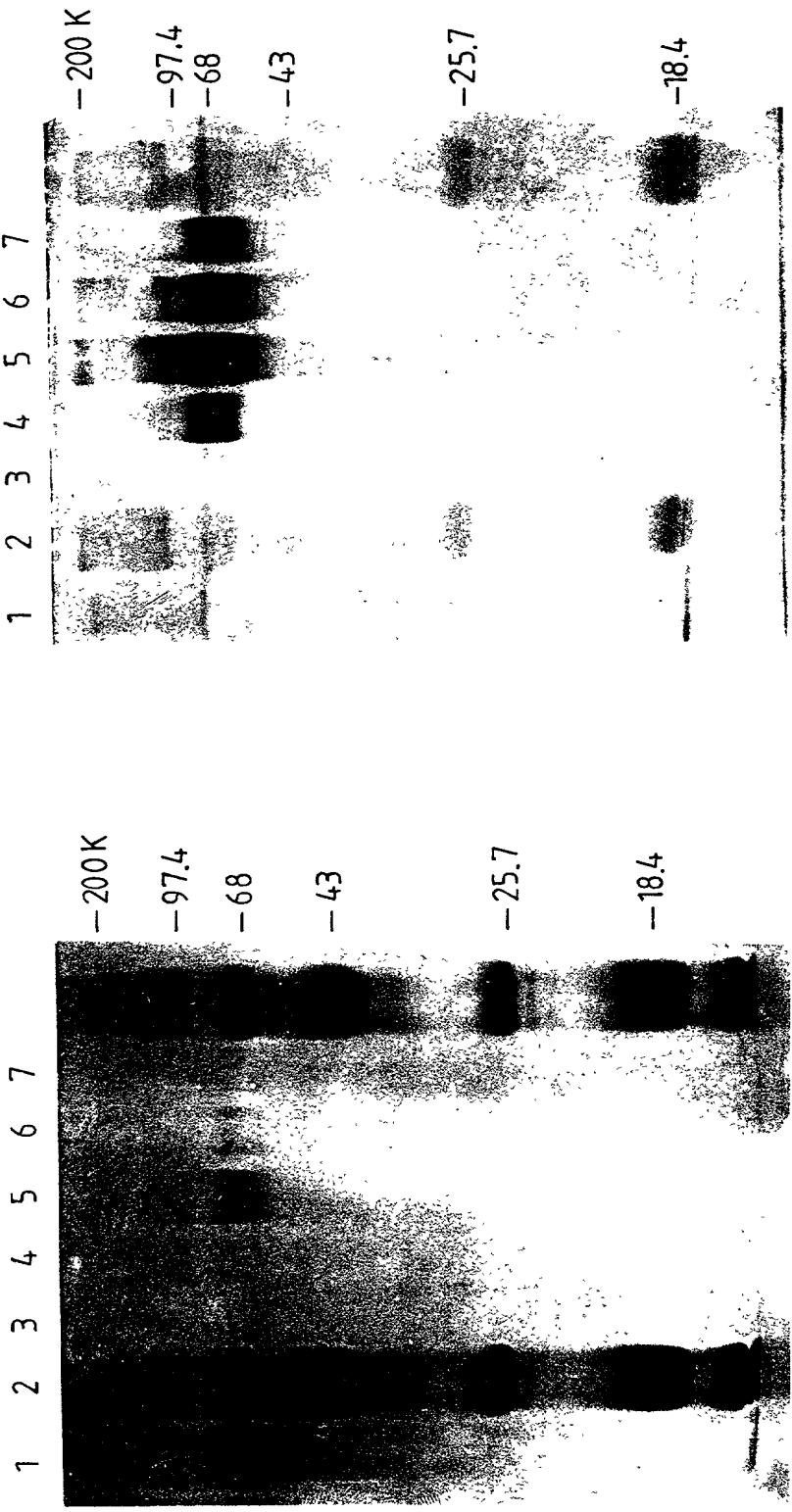


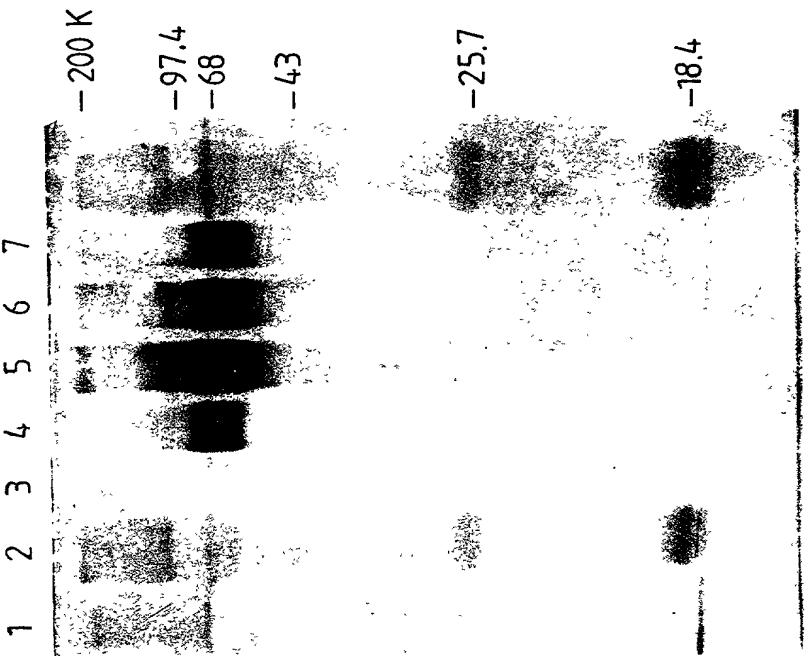
**FIG. 1**



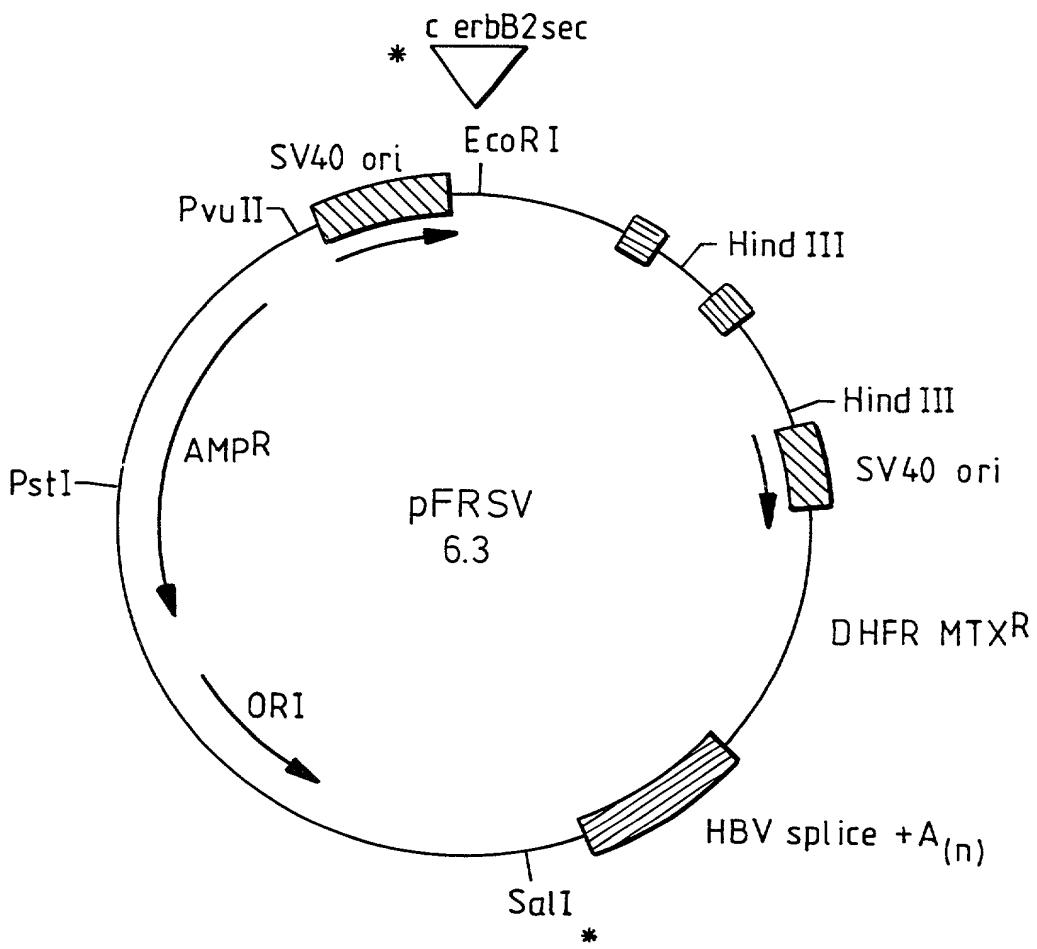
**FIG. 2A**



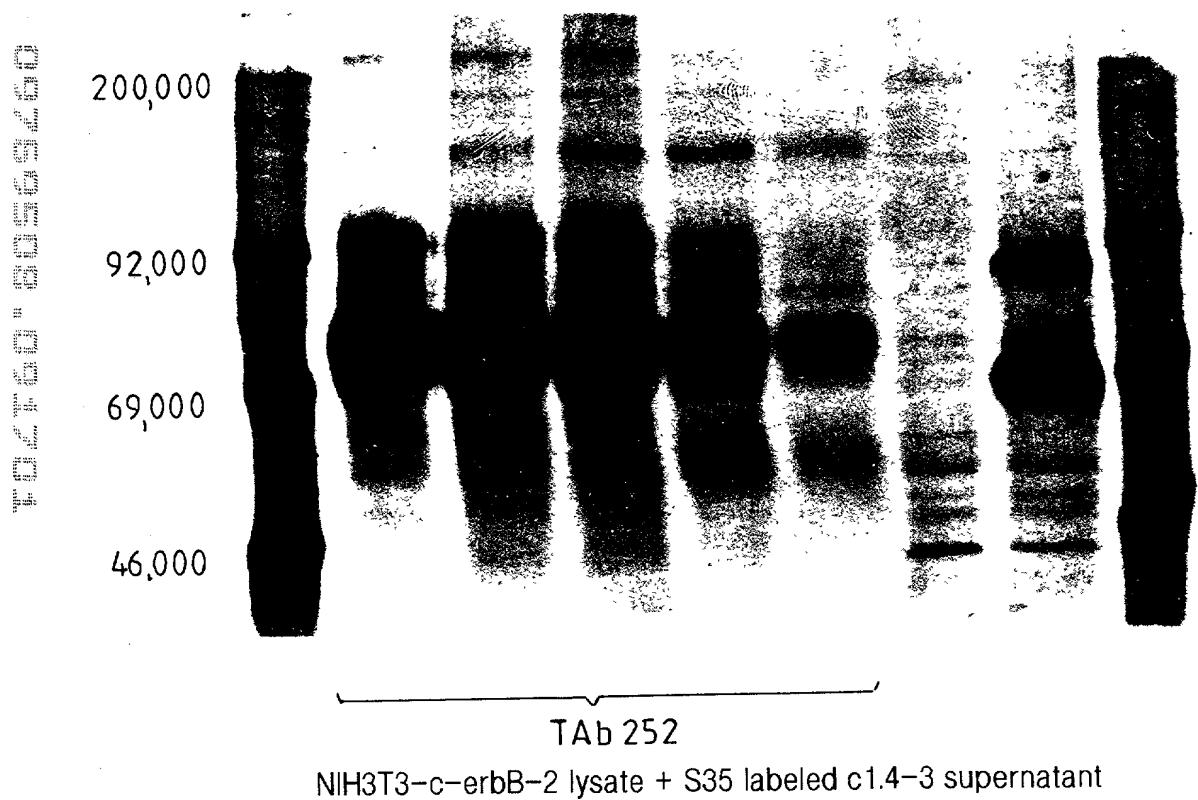
**FIG. 2B**



**FIG. 3**

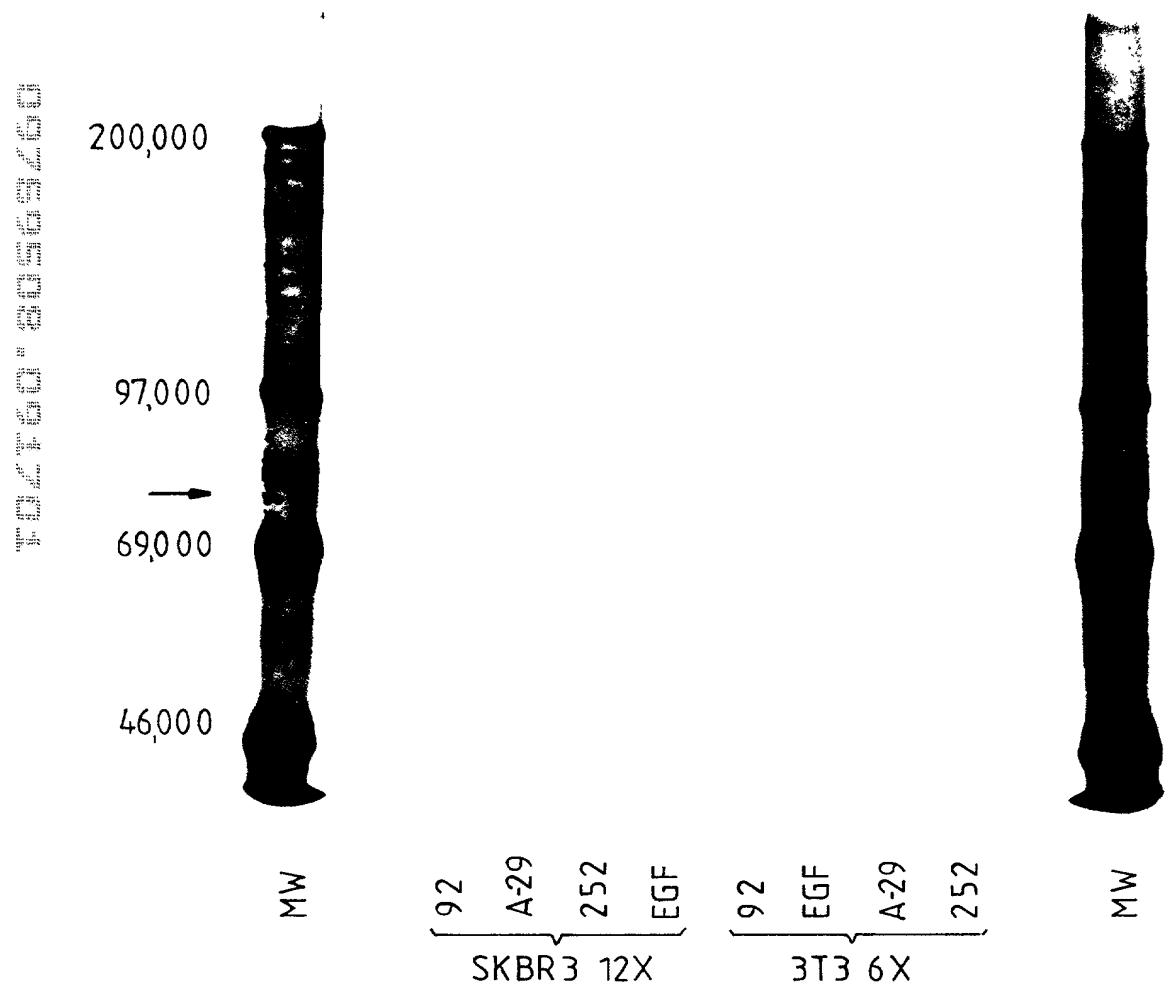


**FIG. 4**



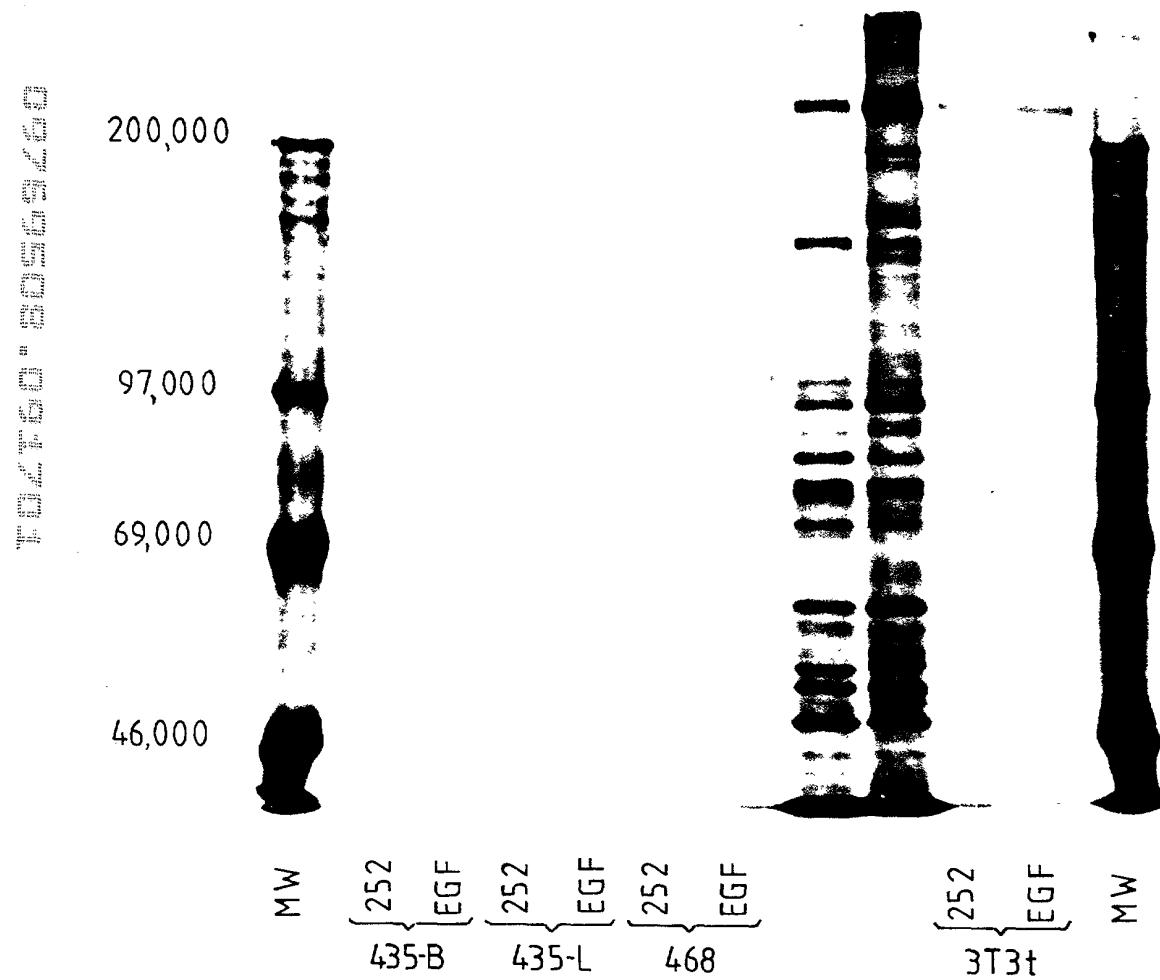
# FIG. 5

Radioimmunoprecipitation of gp75 from SKBR3 Supernatant



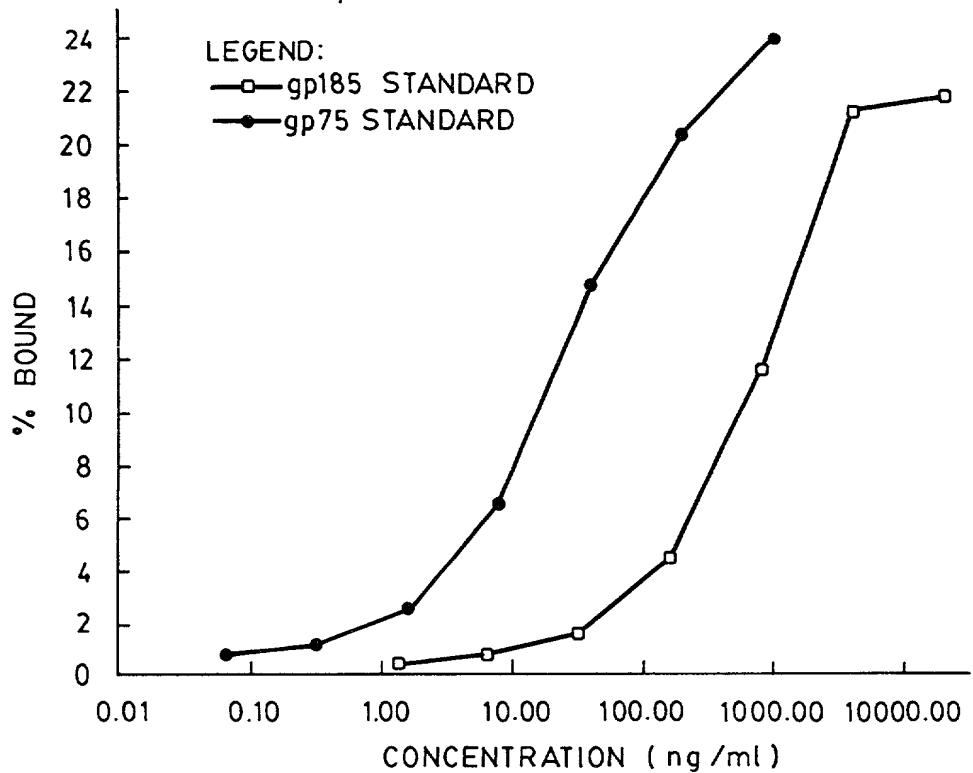
**FIG. 6**

Radioimmunoprecipitation of Supernatants From Various Cell Lines



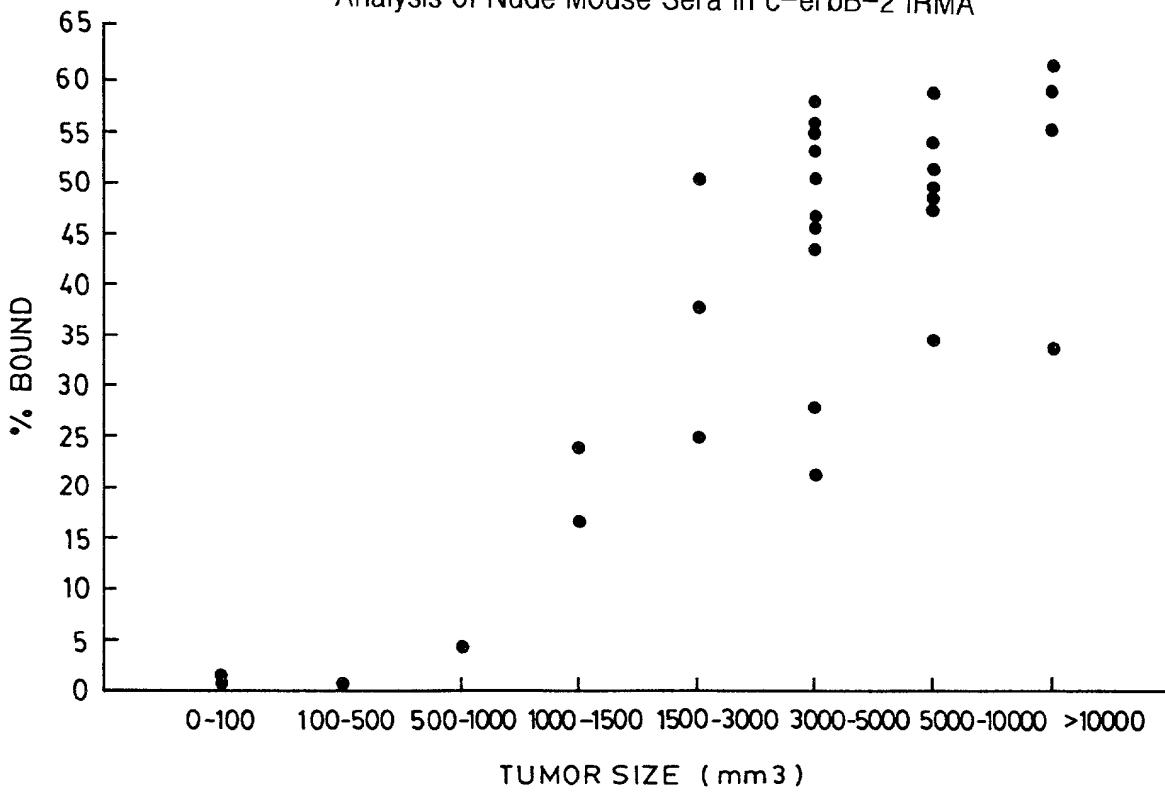
**FIG. 7**

Comparison of Standards in Sandwich IRMA



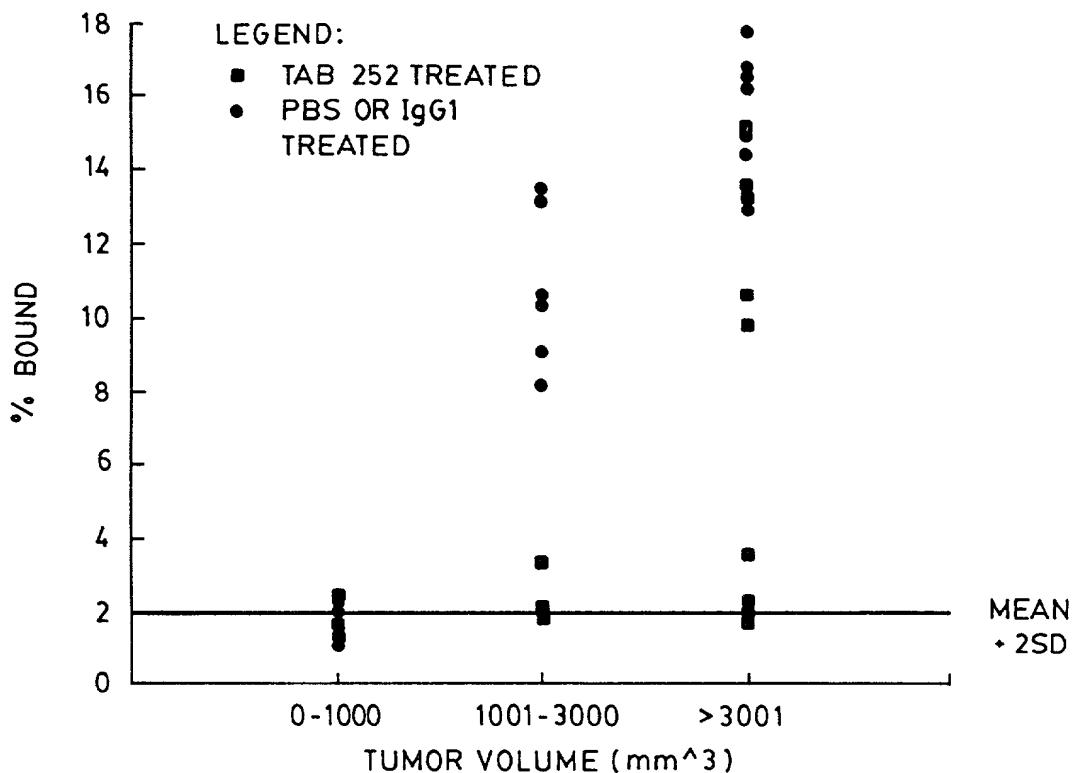
**FIG. 8**

Analysis of Nude Mouse Sera In c-erbB-2 IRMA



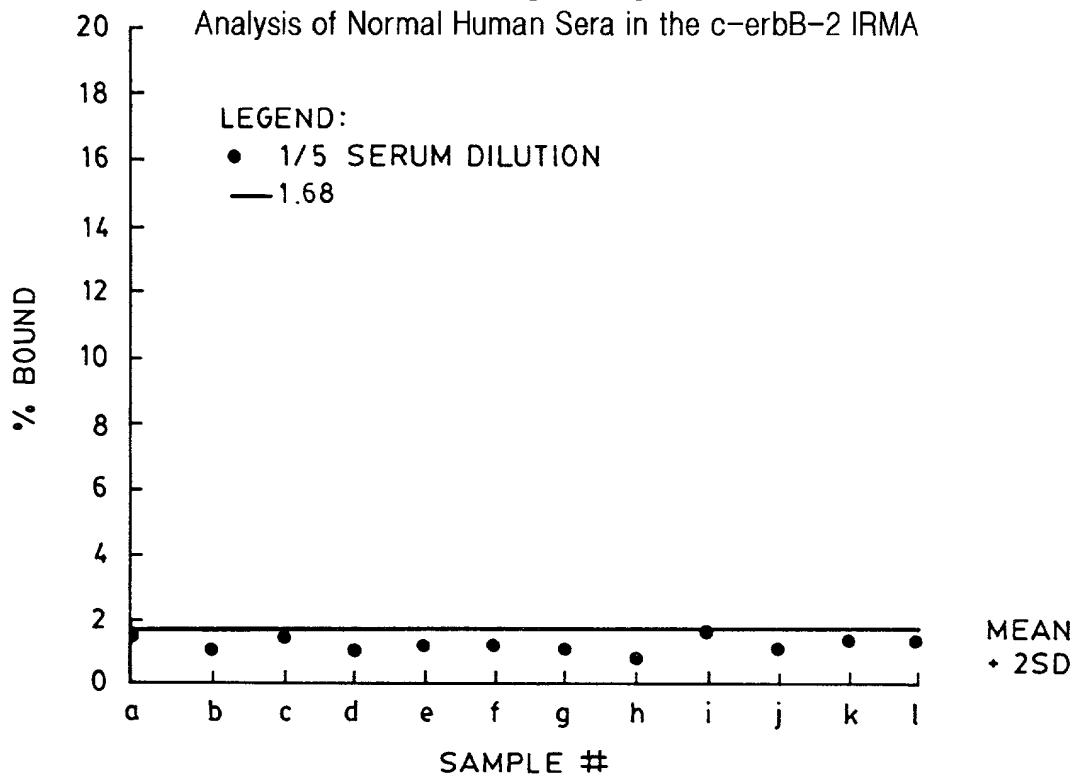
## FIG. 9

Analysis of Nude Mouse Sera in the c-erbB-2 IRMA  
Treated vs. Untreated

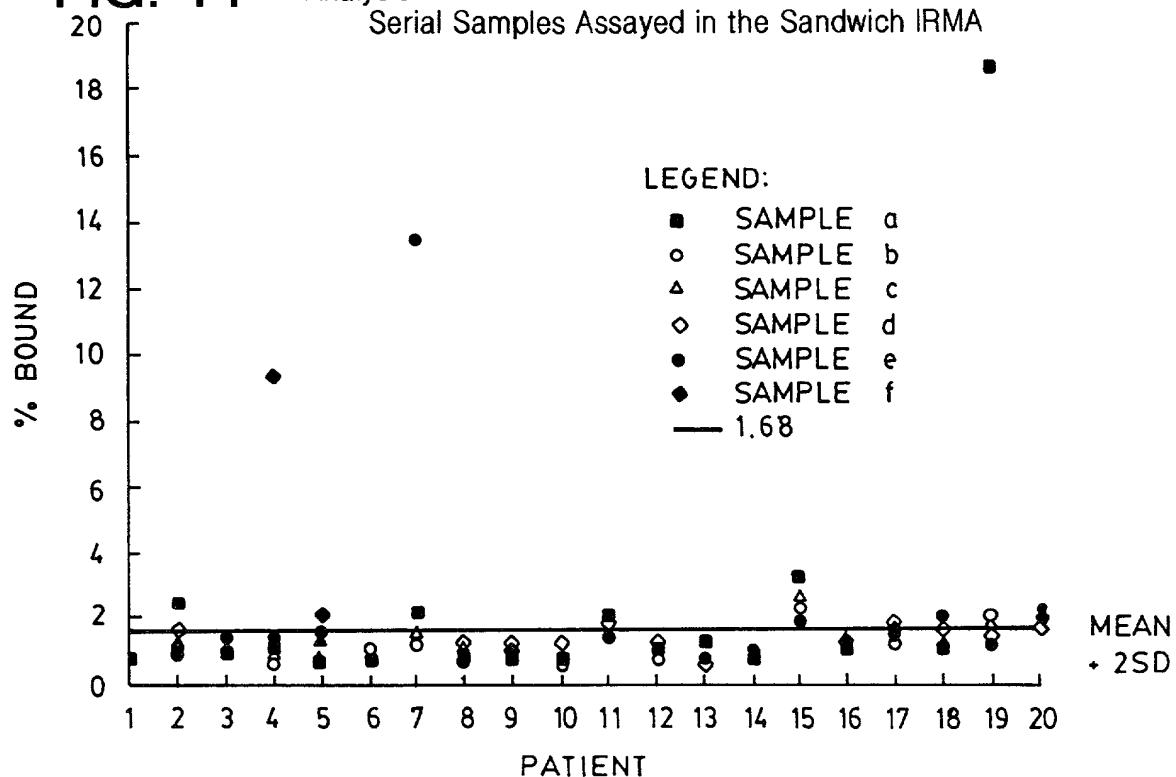


## FIG. 10

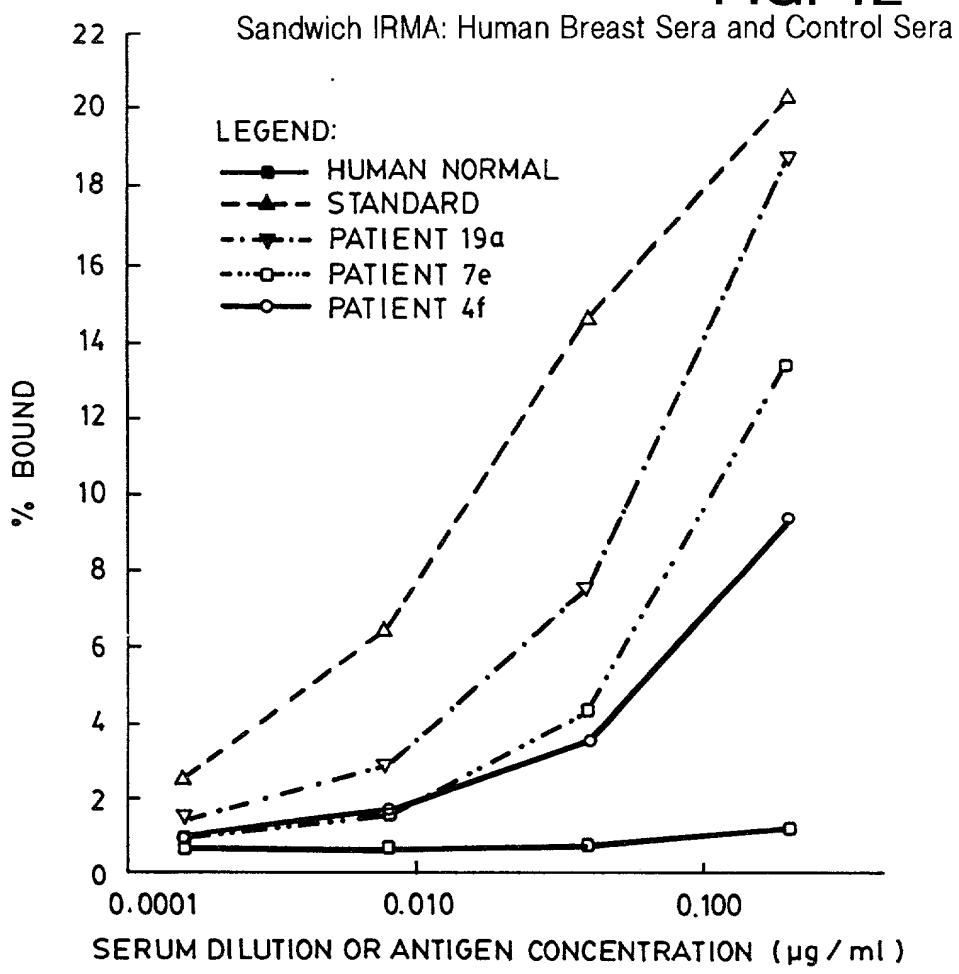
Analysis of Normal Human Sera in the c-erbB-2 IRMA



**FIG. 11** Analysis of 20 Sera from Human Breast Cancer Patients  
Serial Samples Assayed in the Sandwich IRMA

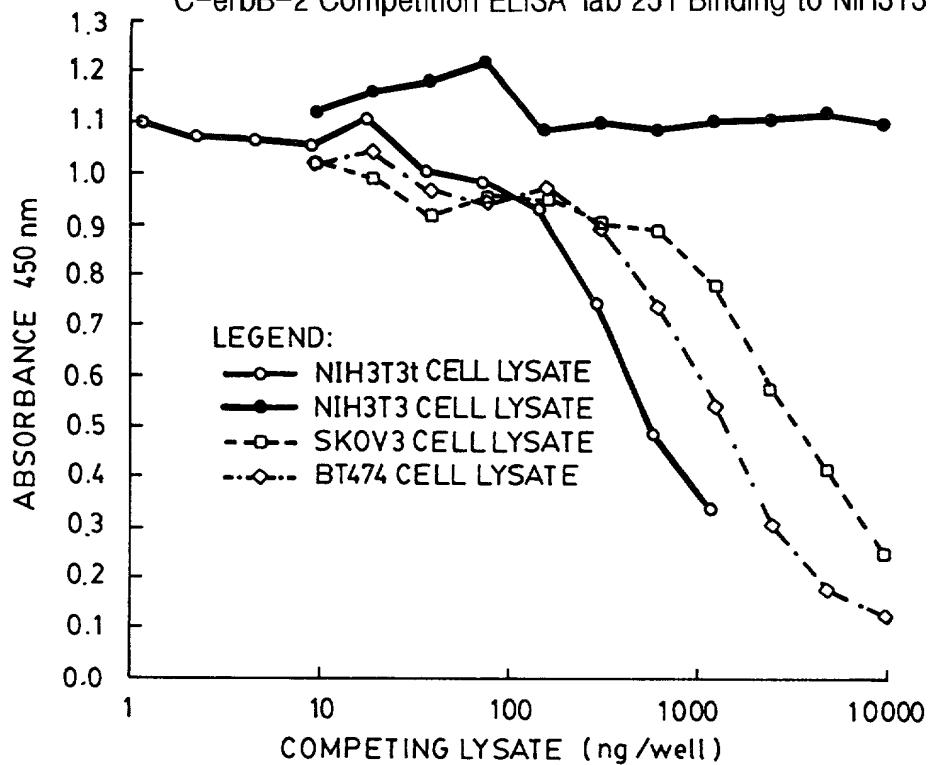


**FIG. 12**



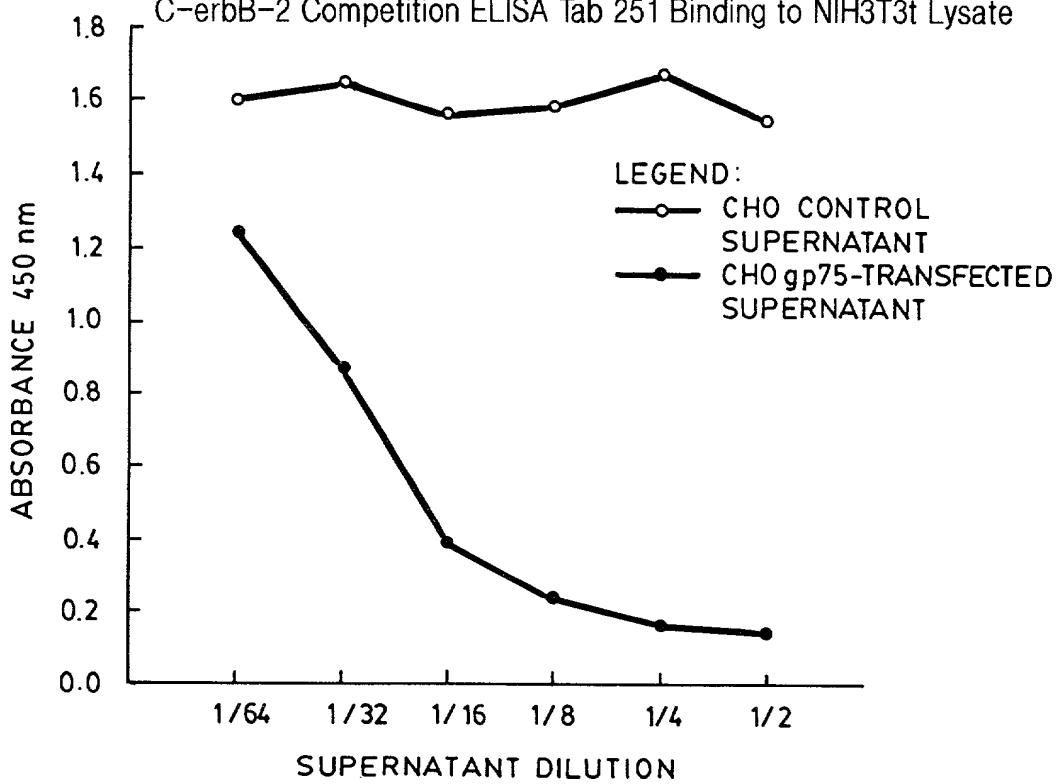
**FIG. 13**

C-erbB-2 Competition ELISA Tab 251 Binding to NIH3T3t Lysate



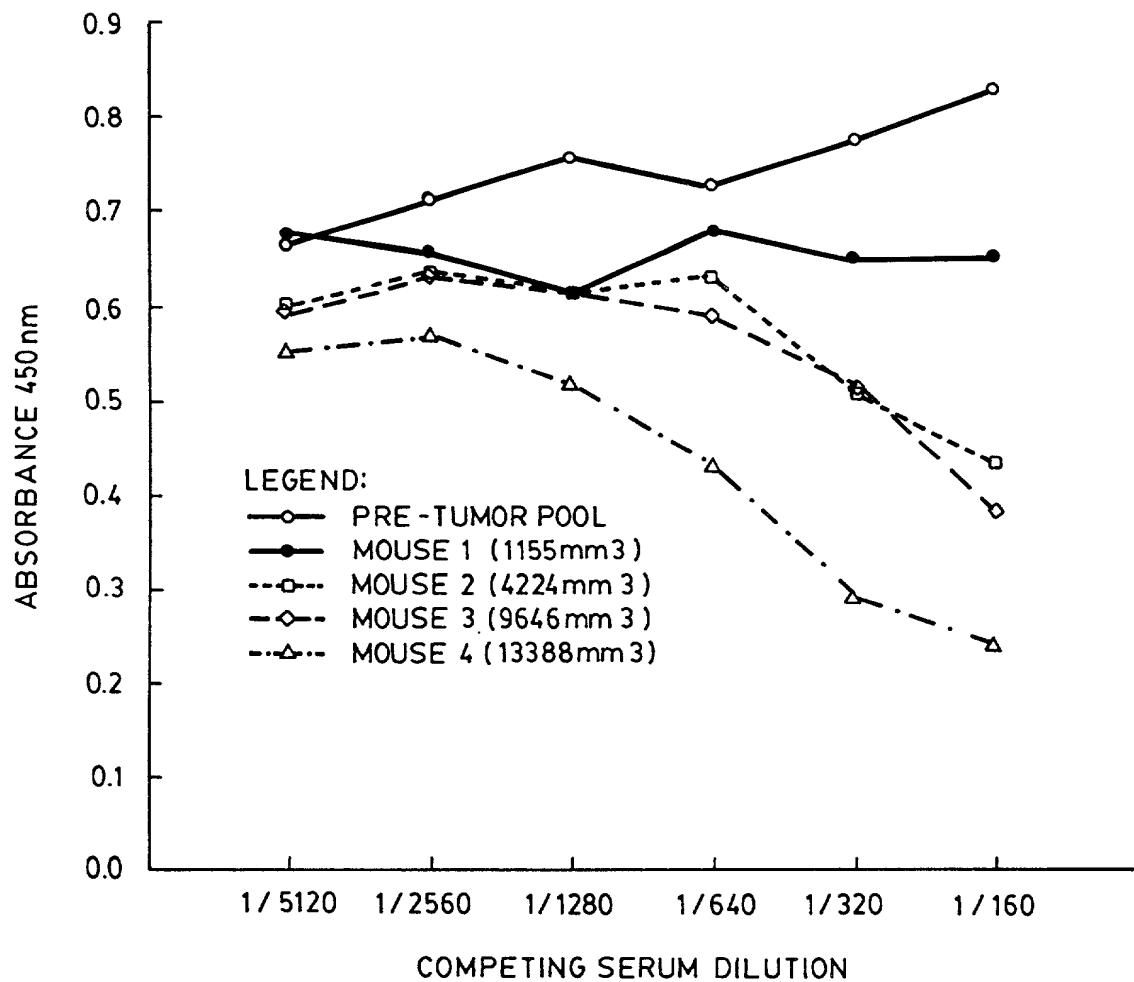
**FIG. 14**

C-erbB-2 Competition ELISA Tab 251 Binding to NIH3T3t Lysate



**FIG. 15**

C-erbB-2 Competition ELISA Tab 251 Binding to NIH3T3t Lysate



1 AATTCTCGAGCTCGTCGACCGGTGACGAGCTCGAGGGTCGACGAGC  
 1 10  
 MetGluLeuAlaAlaLeuCysArgTrpGlyLeuLeuLeuAlaLeuLe  
 151 ATGGAGCTGGCGGCCTTSTGCCGCTGGGGCTCCTCGCCCTCTT  
 60 GlnGlyCysGlnValValGlnGlyAsnLeuGluLeuThrTyrLeuPr  
 301 CAGGGCTGCCAGGTGGTGCAGGGAAACCTGGAACACTCACCTACCTGCC  
 110 IleValArgGlyThrGlnLeuPheGluAspAsnTyrAlaLeuAlaVa  
 451 ATTGTGCGAGGCACCCAGCTCTTGAGGACAACATGCCCTGGCCGT  
 160 GlyGlyValLeuIleGlnArgAsnProGlnLeuCysTyrGlnAspTh  
 601 GGAGGGGTCTTGATCCAGCGGAACCCCCAGCTTGCTACCAGGACAC  
 210 GlySerArgCysTrpGlyGluSerSerGluAspCysGlnSerLeuTh  
 751 GGCTCCCGCTTGCTGGGGAGAGAGTTCTGAGGATTGTCAGAGCCTGAC  
 260 AspCysLeuAlaCysLeuHisPheAsnHisSerGlyIleCysGluLe  
 901 GACTTGCTGGCCTTGCTCCACTCAACCACAGTGGCATTGTGAGCT  
 310 TyrAsnTyrLeuSerThrAspValGlySerCysThrLeuValCysPr  
 1051 TACAAC~~T~~AC~~T~~TTCTACGGACGTGGATTGCTACCCTCGTTGCTGGCC  
 360 ArgGluValARgAlaValThrSerAlaAsnIleGlnGluPheAlaGl  
 1201 CGAGAGGTGAGGGCAGTTACCAGTGCCAATATCCAGGAGTTGCTGG  
 410 GluThrLeuGluGluIleThrGlyTyrLeuTyrIleSerAlaTrpPr  
 1351 GAGACTCTGGAAGAGATCACAGGTTACCTATACTCAGCATGGCC  
 460 SerTrpLeuGlyLeuArgSerLeuArgGluLeuGlySerGlyLeuAl  
 1501 AGCTGGCTGGGGCTGCGCTCACTGAGGGACTGGCAGTGGACTGGC  
 510 GluAspGluCysValGlyGluGlyLeuAlaCysHisGlnLeuCysAl  
 1651 GAGGACGAGTGTGTGGCGAGGGCCTGGCTGCTACCAGCTGTGCGC  
 560 ProArgGluTyrValAsnAlaArgHisCysLeuProCysHisProGl  
 1801 CCCAGGGACTATGTGAATGCCAGGCACTGTTTGCCGTGCCACCCCTGA  
 610 ProSerGlyValLysProAspLeuSerTyrMetProIleTrpLysPh  
 1951 CCCAGCGGTGTGAAACCTGACCTCCTACATGCCCATCTGGAAGTT

FIG. 16A

TCGAGGGCGCGCCGGCCCCACCCCTCGCAGCACCCCGCGCCCCCGC  
20 30  
uProProGlyAlaAlaSerThrGlnValCysThrGlyThrAspMetLysLe  
GCCCCCCCGGAGCCGAGCACCCAAAGTGTGCACCAGCACAGACATGAAGCT  
70 80  
oThrAsnAlaSerLeuSerPheLeuGlnAspIleGlnGluValGlnGlyTy  
CACCAATGCCAGCCTGTCCTCCTGCAGGATATCCAGGAGGTGCAGGGCTA  
120 130  
lLeuAspAsnGlyAspProLeuAsnAsnThrThrProValThrGlyAlaSe  
GCTAGACAATGGAGACCCGCTGAACAATACCACCCCTGTCACAGGGGCCTC  
170 180  
rIleLeuTrpLysAspIlePheHisLysAsnAsnGlnLeuAlaLeuThrLe  
GATTTGTGGAAGGACATCTTCCACAAGAACAAACCAGCTGGCTCTCACACT  
220 230  
rArgThrValCysAlaGlyGlyCysAlaArgCysLysGlyProLeuProTh  
GCGCACTGTCTGTGCCGGTGGCTGTGCCCGCTGCAAGGGGCCACTGCCAC  
270 280  
uHisCysProAlaLeuValThrTyrAsnThrAspThrPheGluSerMetPr  
GCACTGCCAGCCCTGGTCACCTACAACACAGACACGTTGAGTCCATGCC  
320 330  
oLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgCysGluLy  
CCTGCACAACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAA  
370 380  
yCysLysLysIlePheGlySerLeuAlaPheLeuProGluSerPheAspGl  
CTGCAAGAAGATCTTGGAGCCTGGCATTTCTGCCGGAGAGCTTGATGG  
420 430  
oAspSerLeuProAspLeuSerValPheGlnAsnLeuGlnValIleArgGl  
GGACAGCCTGCCTGACCTCAGCGTCTCCAGAACCTGCAAGTAATCCGGGG  
470 480  
aLeuIleHisHisAsnThrHisLeuCysPheValHisThrValProTrpAs  
CCTCATCCACCATAACACCCACCTTGCTTCGCACACGGTCCCCTGGGA  
520 530  
aArgArgAlaLeuLeuGlySerGlyProThrGlnCysValAsnCysSerGl  
CCGCAGGGCACTGCTGGGTCAAGGGCCCACCCAGTGTGTCAACTTGCAGGCCA  
570 580  
uCysGlnProGlnAsnGlySerValThrCysPheGlyProGluAlaAspGl  
GTGTCAAGCCCCAGAATGGCTCAGTGACCTGTTTGGACCGGAGGCTGACCA  
620 630  
eProAspGluGluGlyAlaCysGlnProCysProIleAsnCysThrHisSe  
TCCAGATGAGGAGGGCGCATGCCAGCCTTGCCCCATCAACTTGCAACCCACTC

FIG. 16B

CCTCCCAGCCGGGTCCAGCCGGAGCCATGGGGCCGGAGCCGCAGTGAGCACC  
                         40   50  
 uArgLeuProAlaSerProGluThrHisLeuAspMetLeuArgHisLeuTyr  
 GCGGCTCCCTGCCAGTCCCAGACCCACCTGGACATGCTCCGCCACCTCTAC  
                         90   100  
 rValLeuIleAlaHisAsnGlnValArgGlnValProLeuGlnArgLeuArg  
 CGTGCTCATCGCTCACAAACCAAGTGAGGCAGGTCCCCTGCAGAGGCTGCGG  
                         140   150  
 rProGlyGlyLeuArgGluLeuGlnLeuArgSerLeuThrGluIleLeuLys  
 CCCAGGAGGCCTGCGGGAGCTGCAGCTTCGAAGCCTCACAGAGATCTTGAAA  
                         190   200  
 uIleAspThrAsnArgSerArgAlaCysHisProCysSerProMetCysLys  
 GATAGACACCAACCGCTCTCGGGCCTGCCACCCCTGTTCTCCGATGTGTAAG  
                         240   250  
 rAspCysCysHisGluGlnCysAlaAlaGlyCysThrGlyProLysHisSer  
 TGACTGCTGCCATGAGCAGTGTGCTGCCGGCTGCCACGGGCCCAAGCACTCT  
                         290   300  
 oAsnProGluGlyArgTyrThrPheGlyAlaSerCysValThrAlaCysPro  
 CAATCCCGAGGGCCGGTATACATTGGCGCCAGCTGTGTGACTGCCGTCCC  
                         340   350  
 sCysSerLysProCysAlaArgValCysTyrGlyLeuGlyMetGluHisLeu  
 GTGCAGCAAGCCCTGTGCCCGAGTGTGCTATGGTCTGGCATGGAGCACTTG  
                         390   400  
 yAspProAlaSerAsnThrAlaProLeuGlnProGluGlnLeuGlnValPhe  
 GGACCCAGCCTCCAACACTGCCCGCTCCAGCCAGAGCAGCTCCAAGTGT  
                         440   450  
 yArgIleLeuHisAsnGlyAlaTyrSerLeuThrLeuGlnGlyLeuGlyIle  
 ACGAATTCTGCACAATGGCGCCTACTCGCTGACCCCTGCAAGGGCTGGC  
                         490   500  
 pGlnLeuPheArgAsnProHisGlnAlaLeuLeuHisThrAlaAsnArgPro  
 CCAGCTTTCGGAACCCGCACCAAGCTCTGCTCCACACTGCCAACCGGCCA  
                         540   550  
 nPheLeuArgGlyGlnGluCysValGluGluCysArgValLeuGlnGlyLeu  
 GTTCCTTCGGGAGGAGTGGCTGGAGGAATGCCGAGTACTGCAGGGGCTC  
                         590   600  
 nCysValAlaCysAlaHisTyrLysAspProProPheCysValAlaArgCys  
 GTGTGTGGCCTGTGCCACTATAAGGACCCCTCCCTCTGGCTGGCCCGCTGC  
                         640   650  
 rCysValAspLeuAspAspLysGlyCysProAlaGluGlnArgAlaSerPro  
 CTGTGTGGACCTGGATGACAAGGGCTGCCCGCCGAGCAGAGGCCAGCCCT



FIG. 16C

660

LeuThrSerIleValSerAlaValValGlyIleLeuLeuValValVa  
 2101 CTGACGTCCATCGTCTCTGCGGTGGCATTCTGCTGGTCGTGGT

710

ThrProSerGlyAlaMetProAsnGlnAlaGlnMetArgIleLeuLy  
 2251 ACACCTAGCGGAGCGATGCCAACCAACCAGGCGCAGATGCGGATCCTGAA

760

AlaIleLysValLeuArgGluAsnThrSerProLysAlaAsnLysGl  
 2401 GCCATCAAAGTGGTGGAGGGAAAACACATCCCCAAAGCCAACAAAGA

810

MetProTyrGlyCysLeuLeuAspHisValArgGluAsnArgGlyAr  
 2551 ATGCCCTATGGCTGCCTTAGACCATGTCCGGGAAAACCGCGGACG

860

ValLeuValLysSerProAsnHisValLysIleThrAspPheGlyLe  
 2701 GTGCTGGTCAAGAGTCCAACCATGTCAAAATTACAGACTTCGGGCT

910

HisGlnSerAspValTrpSerTyrGlyValThrValTrpGluLeuMe  
 2851 CACCAGAGTGATGTGTGGAGTTATGGTGTGACTGTGTGGAGCTGAT

△

ValTyrMetIleMetValLysCysTrpMetIleAspSerGluCysAr  
 3001 GTCTACATGATCATGGTCAAATGTGGATGATTGACTCTGAATGTCG

1010

AspSerThrPheTyrArgSerLeuLeuGluAspAspAspMetGlyAs  
 3151 GACAGCACCTTCTACCGCTCACTGCTGGAGGACGATGACATGGGGGA

1060

SerThrArgSerGlyGlyAspLeuThrLeuGlyLeuGluProSe  
 3301 TCTACCAGGAGTGGCGGTGGGACCTGACACTAGGGCTGGAGCCCTC

1110

LeuProThrHisAspProSerProLeuGlnArgTyrSerGluAspPr  
 3451 CTCCCCACACATGACCCCAGCCCTCTACAGCGGTACAGTGAGGACCC

1160

SerProArgGluGlyProLeuProAlaAlaArgProAlaGlyAlaTh  
 3601 TCGCCCCGAGAGGGCCCTCTGCCTGCTGCCGACCTGCTGGTGCCAC

1210

GlyGlyAlaAlaProGlnProHisProProProAlaPheSerProAl  
 3751 GGAGGAGCTGCCCTCAGCCCCACCCCTCCTGCCTTCAGCCCAGC

1255

LeuAspValProValEND

3901 CTGGACGTGCCAGTGTGAACCAGAAGGCCAAGTCCGCAGAACCCCTG

4051 CTAAGGAACCTCCTCCTGCTTGAGTTCCCAGATGGCTGGAAGGGG

4201 CCCTTCCCTCCAGATCCTGGGTACTGAAAGCCTTAGGAAAGCTGGC

4351 ATGGTGTCACTATCCAGGCTTGTACAGAGTGCTTTCTGTTAGTT

4501 TTGTCCATTGCAAATATTTGGAAAACAAAAAA

**FIG. 16D**

670 680  
 1 LeuGlyValValPheGlyIleLeuIleLysArgArgGlnGlnLysIleAr  
 CTTGGGGGTGGTCTTGGGATCCTCATCAAGCGACGGCAGCAGAAGATCCG  
 720 730  
 sGluThrGluLeuArgLysValLysValLeuGlySerGlyAlaPheGlyTh  
 AGAGACGGAGCTGAGGAAGGTGAAGGTGCTTGGATCTGGCGCTTTGGCAC  
 770 780  
 uIleLeuAspGluAlaTyrValMetAlaGlyValGlySerProTyrValSe  
 AATCTTAGACGAAGCATACTGATGGCTGGTGTGGCTCCCCATATGTCTC  
 ▲ 830  
 gLeuGlySerGlnAspLeuLeuAsnTrpCysMetGlnIleAlaLysGlyMe  
 CCTGGGCTCCCAGGACCTGCTGA~~ACTGGTGT~~ATGCAGATTGCCAAGGGGAT  
 870 880 ▲  
 uAlaArgLeuLeuAspIleAspGluThrGluTyrHisAlaAspGlyGlyLy  
 GGCTCGGCTGCTGGACATTGACGAGACAGAGTACCATGCAGATGGGGCAA  
 920 930  
 tThrPheGlyAlaLysProTyrAspGlyIleProAlaArgGluIleProAs  
 GACTTTGGGCCAACCTTACGATGGGATCCCAGCCCAGGAGATCCCTGA  
 970 980  
 gProArgPheArgGluLeuValSerGluPheSerArgMetAlaArgAspPr  
 GCCAAGATTCCGGAGTTGGTGTCTGAATTCTCCGCATGCCAGGGACCC  
 1020 1030  
 pLeuValAspAlaGluGluTyrLeuValProGlnGlnGlyPhePheCysPr  
 CCTGGTGGATGCTGAGGAGTATCTGGTACCCAGCAGGGCTTCTCTGTCC  
 1070 1080  
 rGluGluGluAlaProArgSerProLeuAlaProSerGluGlyAlaGlySe  
 TGAAGAGGAGGCCAGGTCTCCACTGGCACCCCTCCGAAGGGCTGGCTC  
 1120 1130  
 oThrValProLeuProSerGluThrAspGlyTyrValAlaProLeuThrCy  
 CACAGTACCCCTGCCCTCTGAGACTGATGGCTACGTTGCCCTGACCTG  
 1170 1180  
 rLeuGluArgAlaLysThrLeuSerProGlyLysAsnGlyValValLysAs  
 TCTGGAAAGGGCCAAGACTCTCCCCAGGGAGAATGGGGTCGTCAAAGA  
 1220 1230  
 aPheAspAsnLeuTyrTyrTrpAspGlnAspProProGluArgGlyAlaPr  
 CTTCGACAACCTCTATTACTGGGACCAGGACCCACCAGAGCAGGGGGCTCC

ATGTGTCCTCAGGGAGCAGGGAAAGGCCTGACTCTGCTGGCATCAAGAGGT  
TCCAGCCTCGTTGGAAGAGGAACAGCACTGGGGAGTCTTGTGGATTCTGA  
CTGAGAGGGGAAGCGGCCCTAAGGGAGTGTCTAAGAACAAAAGCGACCCAT  
TTTACTTTTTTTGTTTGTGTTTTAAAGACGAAATAAGACCCAGGGGAG

**FIG. 16E**